

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 23:47:23 ; Search time 3832 Seconds
(without alignments)
16974.144 Million cell updates/sec

Title: US-10-055-569A-19
Perfect score: 1785
Sequence: 1 agtccggctcgacct.....aagggtteatgcccttccc 1785

Scoring table: IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues
Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
EST:\*
1: gb\_est1:\*
2: gb\_est2:\*
3: gb\_hc:\*
4: gb\_est3:\*
5: gb\_est4:\*
6: gb\_est5:\*
7: gb\_est6:\*
8: gb\_gsl:\*
9: gb\_gsl2:\*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Table with columns: Result No., Score, Query Match, Length, DB ID, Description. Contains 24 rows of search results.

Table with columns: 25, 466, 26.1, 592, 7, CN347348, 170005321, 26, 441.6, 24.7, 798, 5, BX444974, 4444974, 27, 440.8, 24.7, 4275, 3, BC056941, MUS MUSCU, 28, 438.2, 24.5, 1123, 1, AL563186, AL563186, 29, 430.4, 24.1, 910, 6, CB182208, AGENCOURT, 30, 398.8, 22.3, 641, 2, BB652629, BB652629, 31, 395.4, 22.2, 776, 5, B0884741, AGENCOURT, 32, 388.4, 21.8, 390, 7, CN347353, 170006000, 33, 383.2, 21.5, 689, 6, CB527206, UI-M-PYO, 34, 382.2, 21.4, 700, 6, CB528179, UI-M-PYO, 35, 379, 21.2, 487, 6, CD637986, 56022172J, 36, 379, 21.2, 500, 6, CD637985, 56022172H, 37, 379, 21.2, 506, 6, CD637989, 56022180H, 38, 379, 21.2, 507, 6, CD637990, 56022180J, 39, 379, 21.2, 532, 6, CD638023, 56022280H, 40, 379, 21.2, 537, 6, CD638027, 56022288H, 41, 379, 21.2, 538, 6, CD638028, 56022288J, 42, 379, 21.2, 543, 6, CD637980, 56021810J, 43, 378.4, 21.2, 645, 6, BY709932, BY709932, 44, 375.8, 21.1, 514, 6, CD637993, 56022188H, 45, 375.8, 21.1, 514, 6, CD638032, 56022296J

ALIGNMENTS

RESULT 1 AK049639 2514 bp mRNA linear HTC 03-APR-2004
AK049639 Mus musculus 12 days embryo spinal cord cDNA, RIKEN full-length
LOCUS enriched library, clone:CS30010J15 product:GLYPICAM-2 PRECURSOR
DEFINITION (CEREBROGLYCAN) (HSPG M13) homolog [Rattus norvegicus], full insert
sequence.
ACCESSION AK049639
VERSION AK049639.1 GI:26340377
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1
REFERENCE Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
AUTHORS Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
REFERENCE 10349636
2
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
REFERENCE 11042159
3
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagao, S., Sasaki, N., Carninci, P.,
Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M.,
Sum, N., Ishii, Y., Nakamura, S., Hazama, M., Nishino, T., Harada, A.,
Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K.,
Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M.,
Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,
Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format
sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
REFERENCE 11076861
4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the
FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5

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OM nucleic - nucleic search, using sw model

Run on: November 21, 2004, 18:53:50 ; Search time 5046 Seconds
(without alignments)
16728.520 Million cell updates/sec

Title: US-10-055-569A-19
Perfect score: 1785
Sequence: 1 atgtcgcgctgacacctt.....aagggttcagccctttcc 1785

Scoring table: IDENTITY\_NUC
Gapop 10.0 , Gapext 1.0
Searched: 4526729 seqs, 23644849745 residues
Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

- GenEmbl:\*
1: gb\_ba.\*
2: gb\_bcg.\*
3: gb\_in.\*
4: gb\_om.\*
5: gb\_ov.\*
6: gb\_pat.\*
7: gb\_ph.\*
8: gb\_pl.\*
9: gb\_pr.\*
10: gb\_ro.\*
11: gb\_sts.\*
12: gb\_sy.\*
13: gb\_uni.\*
14: gb\_vi.\*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Table with columns: Result No., Score, Query Match, Length, DB ID, Description. Contains 19 rows of search results.

Table with columns: RESULT, LOCUS, DEFINITION, ACCESSION, VERSION, SOURCE, ORGANISM, REFERENCE, AUTHORS, TITLE, JOURNAL, FEATURES, ORIGIN, Query Match, Best Local Similarity, Matches. Contains 45 rows of sequence data.

ALIGNMENTS

Table showing sequence alignments for various species including Homo sapiens, Mus musculus, and others. Includes alignment scores and identifiers.

